

SEQUENCE LISTING

<110> Luo, Ying
Xu, Xiang
Rigel Pharmaceuticals, Inc.

<120> Novel TRAF4 Associated Cell Cycle Proteins,
Compositions and Methods of Use

<130> 021044-004810US

<140> US 10/088,961

<141> Not yet assigned

<150> US 09/404,010

<151> 1999-09-23

<150> WO PCT/US00/40987

<151> 2000-09-25

<160> 17

<170> PatentIn Ver. 2.1

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<223> cell cycle protein Mkinase

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cell cycle protein Mkinase

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Arg Asp Phe Pro Phe Glu Leu Ile Pro Glu Pro Pro Glu Gly Gly Leu
35 40 45

Pro Gly Pro Trp Ala Leu His Arg Gly Arg Lys Lys
 50 55 60

Pro Val Ser Ile Phe Val Tyr Asp Val Lys Pro Gly Ala Glu Glu Gln
 65 70 75 80

Thr Gln Val Ala Lys Ala Ala Phe Lys Arg Phe Lys Thr Leu Arg His
 85 90 95

Pro Asn Ile Leu Ala Tyr Ile Asp Gly Leu Glu Thr Glu Lys Cys Leu
 100 105 110

His Val Val Thr Glu Ala Val Thr Pro Leu Gly Ile Tyr Leu Lys Ala
 115 120 125

Arg Val Glu Ala Gly Gly Leu Lys Glu Leu Glu Ile Ser Trp Gly Leu
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His Gln Ile Val Lys Ala Leu Ser Phe Leu Val Asn Asp Cys Ser Leu
145 150 155 160

Ile His Asn Asn Val Cys Met Ala Ala Val Phe Val Asp Arg Ala Gly
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Glu Trp Lys Leu Gly Gly Leu Asp Tyr Met Tyr Ser Ala Gln Gly Asn
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Gly Gly Gly Pro Pro Arg Lys Gly Ile Pro Glu Leu Glu Gln Tyr Asp
195 200 205

Pro Pro Glu Leu Ala Asp Ser Ser Gly Arg Val Val Arg Glu Lys Trp
210 215 220

Ser Ala Asp Met Trp Arg Leu Gly Cys Leu Ile Trp Glu Val Phe Asn
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Gly Pro Leu Pro Arg Ala Ala Ala Leu Arg Asn Pro Gly Lys Ile Pro
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Lys Thr Leu Ala Pro His Tyr Cys Glu Leu Val Gly Ala Asn Pro Lys
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Val Arg Pro Asn Pro Ala Arg Phe Leu Gln Asn Cys Arg Ala Pro Gly
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Gly Phe Met Ser Asn Arg Phe Val Glu Thr Asn Leu Phe Leu Glu Glu
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Ile Gln Ile Lys Glu Pro Ala Glu Lys Gln Lys Phe Phe Gln Glu Leu
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Ser Lys Ser Leu Asp Ala Phe Pro Glu Asp Phe Cys Arg His Lys Leu
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Val Leu Thr Pro Leu Phe Lys Val Gly Lys Phe Leu Ser Ala Glu Glu
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Tyr Gln Gln Lys Ile Ile Pro Val Val Val Lys Met Phe Ser Ser Thr
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Asp Arg Ala Met Arg Ile Arg Leu Leu Gln Gln Met Glu Gln Phe Ile
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Gln Tyr Leu Asp Glu Pro Thr Val Asn Thr Gln Ile Phe Pro His Val
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Val His Gly Phe Leu Asp Thr Asn Pro Ala Ile Arg Glu Gln Thr Val
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Lys Ser Met Leu Leu Leu Ala Pro Lys Leu Asn Glu Ala Asn Leu Asn
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Ala Gly Trp Ala Val Thr Gly Val Ser Ser Leu Thr Ser Lys Leu Ile
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<213> Artificial Sequence

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destruction box

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<212> PRT
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destruction box

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<212> PRT
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destruction box

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<213> Artificial Sequence

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destruction box

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destruction box

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destruction box

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<212> PRT
<213> Artificial Sequence

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destruction box

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Val Lys Leu Ala Lys His Val Ile Thr Gly His Glu Val Ala Ile Lys
   35          40          45

Ile Ile Asp Lys Thr Ala Leu Asn Pro Ser Ser Leu Gln Lys Leu Phe
   50          55          60

Arg Glu Val Lys Ile Met Lys Gln Leu Asp His Pro Asn Ile Val Lys
   65          70          75          80

Leu Tyr Gln Val Met Glu Thr Glu Gln Thr Leu Tyr Leu Val Leu Glu
   85          90          95

Tyr Ala Ser Gly Gly Glu Val Phe Asp Tyr Leu Val Ala His Gly Arg
  100         105         110

Met Lys Glu Lys Glu Ala Arg Ala Lys Phe Arg Gln Ile Val Ser Ala
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Val Gln Tyr Leu His Ser Lys Asn Ile Ile His Arg Asp Leu Lys Ala
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Glu Asn Leu Leu Leu Asp Gln Asp Met Asn Ile Lys Ile Ala Asp Phe
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Gly Phe Ser Asn Thr Phe Ser Leu Gly Asn Lys Leu Asp Thr Phe Cys
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Gly Ser Pro Pro Tyr Ala Ala Pro Glu Leu Phe Ser Gly Lys Lys Tyr
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Asp Gly Pro Glu Val Asp Val Trp Ser Leu Gly Val Ile Leu Tyr Thr
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Arg Glu Arg Val Leu Arg
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35 40 45

Ile Ile Asp Lys Thr Gln Leu Asn Pro Thr Ser Leu Gln Lys Leu Phe
50 55 60

Arg Glu Val Arg Ile Met Lys Ile Leu Asn His Pro Asn Ile Val Lys
65 70 75 80

Leu Phe Glu Val Ile Glu Thr Glu Lys Thr Leu Tyr Leu Val Met Glu
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Tyr Ala Ser Gly Gly Glu Val Phe Asp Tyr Leu Val Ala His Gly Arg
100 105 110

Met Lys Glu Lys Glu Ala Arg Ala Lys Phe Arg Gln Ile Val Ser Ala
115 120 125

Val Gln Tyr Cys His Gln Lys Tyr Ile Val His Arg Asp Leu Lys Ala
130 135 140

Glu Asn Leu Leu Asp Gly Asp Met Asn Ile Lys Ile Ala Asp Phe
145 150 155 160

Gly Phe Ser Asn Glu Phe Thr Val Gly Asn Lys Leu Asp Thr Phe Cys
165 170 175

Gly Ser Pro Pro Tyr Ala Ala Pro Glu Leu Phe Gln Gly Lys Lys Tyr
180 185 190

Asp Gly Pro Glu Val Asp Val Trp Ser Leu Gly Val Ile Leu Tyr Thr
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Arg Glu Arg Val Leu Arg
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Gly Asn Tyr Arg Leu Leu Lys Thr Ile Gly Lys Gly Asn Phe Ala Lys
20 25 30

Val Lys Leu Ala Arg His Ile Leu Thr Gly Lys Glu Val Ala Val Lys
35 40 45

Ile Ile Asp Lys Thr Gln Leu Asn Ser Ser Ser Leu Gln Lys Leu Phe
50 55 60

Arg Glu Val Arg Ile Met Lys Val Leu Asn His Pro Asn Ile Val Lys
65 70 75 80

Leu Phe Glu Val Ile Glu Thr Glu Lys Thr Leu Tyr Leu Val Met Glu
85 90 95

Tyr Ala Ser Gly Gly Glu Val Phe Asp Tyr Leu Val Ala His Gly Arg
100 105 110

Met Lys Glu Lys Glu Ala Arg Ala Lys Phe Arg Gln Ile Val Ser Ala
115 120 125

Val Gln Tyr Cys His Gln Lys Phe Ile Val His Arg Asp Leu Lys Ala
130 135 140

Glu Asn Leu Leu Asp Ala Asp Met Asn Ile Lys Ile Ala Asp Phe
145 150 155 160

Gly Phe Ser Asn Glu Phe Thr Phe Gly Asn Lys Leu Asp Thr Phe Cys
165 170 175

Gly Ser Pro Pro Tyr Ala Ala Pro Glu Leu Phe Gln Gly Lys Lys Tyr
180 185 190

Asp Gly Pro Glu Val Asp Val Trp Ser Leu Gly Val Ile Leu Tyr Thr
195 200 205

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Arg Glu Arg Val Leu Arg
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Lys Glu Ile Asn Ile Ser Arg Met Ser Asp Lys Glu Arg Gln Glu Ser
35 40 45

Arg Arg Glu Val Ala Val Leu Ala Asn Met Lys His Pro Asn Ile Val
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Gln Tyr Lys Glu Ser Phe Glu Glu Asn Gly Ser Leu Tyr Ile Val Met
65 70 75 80

Asp Tyr Cys Glu Gly Gly Asp Leu Phe Lys Arg Ile Asn Ala Gln Lys
85 90 95

Gly Ala Leu Phe Gln Glu Asp Gln Ile Leu Asp Trp Phe Val Gln Ile
100 105 110

Cys Leu Ala Leu Lys His Val His Asp Arg Lys Ile Leu His Arg Asp
115 120 125

Ile Lys Ser Gln Asn Ile Phe Leu Thr Lys Asp Gly Thr Val Gln Leu
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Gly Asp Phe Gly Ile Ala Arg Val Leu Asn Ser Thr Val Glu Leu Ala
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Arg Thr Cys Ile Gly Thr Pro Tyr Tyr Leu Ser Pro Glu Ile Cys Glu
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Asn Lys Pro Tyr Asn Asn Lys Ser Asp Ile Trp Ala Leu Gly Cys Val
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35 40 45

Asp Val Lys Pro Gly Ala Glu Glu Gln Thr Gln Val Ala Lys Ala Ala
50 55 60

Phe Lys Arg Phe Lys Thr Leu Arg His Pro Asn Ile Leu Ala Tyr Ile
 65 70 75 80

Asp Gly Leu Glu Thr Glu Lys Cys Leu His Val Val Thr Glu Ala Val
 85 90 95

Thr Pro Leu Gly Ile Tyr Leu Lys Ala Arg Val Glu Ala Gly Leu
 100 105 110

Lys Glu Leu Glu Ile Ser Trp Gly Leu His Gln Ile Val Lys Ala Leu
 115 120 125

Ser Phe Leu Val Asn Asp Cys Ser Leu Ile His Asn Asn Val Cys Met
 130 135 140

Ala Ala Val Phe Val Asp Arg Ala Gly Glu Trp Lys Leu Gly Gly Leu
 145 150 155 160

Asp Tyr Met Tyr Ser Ala Gln Gly Asn Gly Gly Gly Pro Pro Arg Lys
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Gly Ile Pro Glu Leu Glu Gln Tyr Asp Pro Pro Glu Leu Ala Asp Ser
 180 185 190

Ser Gly Arg Val Val Arg Glu Lys Trp Ser Ala Asp Met Trp Arg Leu
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Ala Leu Arg Asn Pro Gly Lys Ile Pro
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<223> Description of Artificial Sequence:kinase
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<212> PRT

<213> Artificial Sequence

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<213> Artificial Sequence

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<223> Description of Artificial Sequence:kinase
"homologue" domain consensus peptide

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SEQUENCE LISTING

<110> Luo, Ying
Xu, Xiang
Rigel Pharmaceuticals, Inc.

<120> Novel TRAF4 Associated Cell Cycle Proteins, Compositions and Methods of Use

<130> 021044-004810US

<140> US 10/088,961

<141> Not yet assigned

<150> US 09/494,919

<151> 1999-09-23

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≤160≥ 17

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<233> cell cycle protein Mkinase

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 cell cycle protein Mkinase

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 20 25 30

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 35 40 45

Pro Gly Pro Trp Ala Leu His Arg Gly Arg Lys Lys Ala Thr Gly Ser
 50 55 60

Pro Val Ser Ile Phe Val Tyr Asp Val Lys Pro Gly Ala Glu Glu Gln
 65 70 75 80

Thr Gln Val Ala Lys Ala Ala Phe Lys Arg Phe Lys Thr Leu Arg His
 85 90 95

Pro Asn Ile Leu Ala Tyr Ile Asp Gly Leu Glu Thr Glu Lys Cys Leu
 100 105 110

His Val Val Thr Glu Ala Val Thr Pro Leu Gly Ile Tyr Leu Lys Ala
 115 120 125

Arg Val Glu Ala Gly Gly Leu Lys Glu Leu Glu Ile Ser Trp Gly Leu
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His Gln Ile Val Lys Ala Leu Ser Phe Leu Val Asn Asp Cys Ser Leu
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Ile His Asn Asn Val Cys Met Ala Ala Val Phe Val Asp Arg Ala Gly
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 Ser Ala Asp Met Trp Arg Leu Gly Cys Leu Ile Trp Glu Val Phe Asn
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 Gly Pro Leu Pro Arg Ala Ala Leu Arg Asn Pro Gly Lys Ile Pro
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 Lys Thr Leu Ala Pro His Tyr Cys Glu Leu Val Gly Ala Asn Pro Lys
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 Val Arg Pro Asn Pro Ala Arg Phe Leu Gln Asn Cys Arg Ala Pro Gly
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 Val Leu Thr Pro Leu Phe Lys Val Gly Lys Phe Leu Ser Ala Glu Glu
 355 360 365
 Tyr Gln Gln Lys Ile Ile Pro Val Val Val Lys Met Phe Ser Ser Thr
 370 375 380
 Asp Arg Ala Met Arg Ile Arg Leu Leu Gln Gln Met Glu Gln Phe Ile
 385 390 395 400
 Gln Tyr Leu Asp Glu Pro Thr Val Asn Thr Gln Ile Phe Pro His Val
 405 410 415
 Val His Gly Phe Leu Asp Thr Asn Pro Ala Ile Arg Glu Gln Thr Val
 420 425 430
 Lys Ser Met Leu Leu Ala Pro Lys Leu Asn Glu Ala Asn Leu Asn
 435 440 445
 Val Glu Leu Met Lys His Phe Ala Arg Leu Gln Ala Lys Asp Glu Gln
 450 455 460
 Gly Pro Ile Arg Cys Asn Thr Thr Val Cys Leu Gly Lys Ile Gly Ser
 465 470 475 480

Tyr Leu Ser Ala Ser Thr Arg His Arg Val Leu Thr Ser Ala Phe Ser
485 490 495

Arg Ala Thr Arg Asp Pro Phe Ala Pro Ser Arg Val Ala Gly Val Leu
500 505 510

Gly Phe Ala Ala Thr His Asn Leu Tyr Ser Met Asn Asp Cys Ala Gln
515 520 525

Lys Ile Leu Pro Val Leu Cys Gly Leu Thr Val Asp Pro Glu Lys Ser
530 535 540

Val Arg Asp Gln Ala Phe Lys Ala Phe Arg Ser Phe Leu Ser Lys Leu
545 550 555 560

Glu Ser Val Ser Glu Asp Pro Thr Gln Leu Glu Glu Val Glu Lys Asp
565 570 575

Val His Ala Ala Ser Ser Pro Gly Met Gly Gly Ala Ala Ser Trp
580 585 590

Ala Gly Trp Ala Val Thr Gly Val Ser Ser Leu Thr Ser Lys Leu Ile
595 600 605

Arg Ser His Pro Thr Thr Ala Pro Thr Glu Thr Asn Ile Pro Gln Arg
610 615 620

Pro Thr Pro Glu Gly Val Pro Ala Pro Ala Pro Thr Pro Val Pro Ala
625 630 635 640

Thr Pro Thr Thr Ser Gly His Trp Glu Thr Gln Glu Glu Asp Lys Asp
645 650 655

Thr Ala Glu Asp Ser Ser Thr Ala Asp Arg Trp Asp Asp Glu Asp Trp
660 665 670

Gly Ser Leu Glu Gln Glu Ala Glu Ser Val Leu Ala Gln Gln Asp Asp
675 680 685

Trp Ser Thr Gly Gly Gln Val Ser Arg Ala Ser Gln Val Ser Asn Ser
690 695 700

Asp His Lys Ser Ser Lys Ser Pro Glu Ser Asp Trp Ser Ser Trp Glu
705 710 715 720

Ala Glu Gly Ser Trp Glu Gln Gly Trp Gln Glu Pro Ser Ser Gln Glu
725 730 735

Pro Pro Ser Asp Gly Thr Arg Leu Ala Ser Glu Tyr Asn Trp Gly Gly
740 745 750

Pro Glu Ser Ser Asp Lys Gly Asp Pro Phe Ala Thr Leu Ser Ala Arg
755 760 765

Pro Ser Thr Gln Pro Arg Pro Asp Ser Trp Gly Glu Asp Asn Trp Glu
770 775 780

Gly Leu Glu Thr Asp Ser Arg Gln Val Lys Ala Glu Leu Ala Arg Lys
785 790 795 800

Lys Arg Glu Glu Arg Arg Glu Met Glu Ala Lys Arg Ala Glu Arg
805 810 815

Lys Val Ala Lys Gly Pro Met Lys Leu Gly Ala Arg Lys Leu Asp
820 825 830

<210> 3

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:cyclin A
destruction box

<400> 3

Arg Thr Val Leu Gly Val Ile Gly Asp
1 5

<210> 4

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:cyclin B1
destruction box

<400> 4

Arg Thr Ala Leu Gly Asp Ile Gly Asn
1 5

<210> 5

<211> 27

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:rat cyclin B
destruction box

<400> 5

Tyr Met Thr Val Ser Ile Ile Asp Arg Phe Met Gln Asp Ser Cys Val
1 5 10 15

Pro Lys Lys Met Leu Gln Leu Val Gly Val Thr
20 25

<210> 6

<211> 28

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:mouse cyclin B
destruction box

<400> 6
Lys Phe Arg Leu Leu Gln Glu Thr Met Tyr Met Thr Val Ser Ile Ile
1 5 10 15

Asp Arg Phe Met Gln Asn Ser Cys Val Pro Lys Lys
20 25

<210> 7
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mouse cyclin B1
destruction box

<400> 7
Arg Ala Ile Leu Ile Asp Trp Leu Ile Gln Val Gln Met Lys Phe Arg
1 5 10 15

Leu Leu Gln Glu Thr Met Tyr Met Thr Val Ser
20 25

<210> 8
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mouse cyclin B2
destruction box

<400> 8
Asp Arg Phe Leu Gln Ala Gln Leu Val Cys Arg Lys Lys Leu Gln Val
1 5 10 15

Val Gly Ile Thr Ala Leu Leu Ala Ser Lys
20 25

<210> 9
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mouse cyclin A2
destruction box

<400> 9
Met Ser Val Leu Arg Gly Lys Leu Gln Leu Val Gly Thr Ala Ala Met
1 5 10 15

Leu Leu

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<210> 10
<211> 230
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:GenBank
      AAA83272 and AAA947437 kinase "homologue" domain

<400> 10
Met Ser Ser Arg Ser Ala Ala Arg Arg Asn Asp Gln Asp Val His Val
 1           5           10           15

Gly Lys Tyr Lys Leu Leu Lys Thr Ile Gly Lys Gly Asn Phe Ala Lys
 20          25           30

Val Lys Leu Ala Lys His Val Ile Thr Gly His Glu Ala Val Ile Lys
 35           40           45

Ile Ile Asp Lys Thr Ala Leu Asn Pro Ser Ser Leu Gln Lys Leu Phe
 50           55           60

Arg Glu Val Lys Ile Met Lys Gln Leu Asp His Pro Asn Ile Val Lys
 65           70           75           80

Leu Tyr Gln Val Met Glu Thr Glu Gln Thr Leu Tyr Leu Val Leu Glu
 85           90           95

Tyr Ala Ser Gly Gly Glu Val Phe Asp Tyr Leu Val Ala His Gly Arg
100          105          110

Met Lys Glu Lys Glu Ala Arg Ala Lys Phe Arg Gln Ile Val Ser Ala
115          120          125

Val Gln Tyr Leu His Ser Lys Asn Ile Ile His Arg Asp Leu Lys Ala
130          135          140

Glu Asn Leu Leu Leu Asp Gln Asp Met Asn Ile Lys Ile Ala Asp Phe
145          150          155          160

Gly Phe Ser Asn Thr Phe Ser Leu Gly Asn Lys Leu Asp Thr Phe Cys
165          170          175

Gly Ser Pro Pro Tyr Ala Ala Pro Glu Leu Phe Ser Gly Lys Lys Tyr
180          185          190

Asp Gly Pro Glu Val Asp Val Trp Ser Leu Gly Val Ile Leu Tyr Thr
195          200          205

Leu Val Ser Gly Ser Leu Pro Phe Asp Gly Gln Asn Leu Lys Glu Leu
210          215          220

Arg Glu Arg Val Leu Arg
225          230

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<210> 11
<211> 230
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:GenBank
AAF72103/MAPK kinase "homologue" domain

<400> 11
Arg Cys Arg Asn Ser Ile Thr Ser Ala Thr Asp Glu Gln Pro His Ile
1 5 10 15

Gly Asn Tyr Arg Leu Gln Lys Thr Ile Gly Lys Gly Asn Phe Ala Lys
20 25 30

Val Lys Leu Ala Arg His Val Leu Thr Gly Arg Glu Val Ala Val Lys
35 40 45

Ile Ile Asp Lys Thr Gln Leu Asn Pro Thr Ser Leu Gln Lys Leu Phe
50 55 60

Arg Glu Val Arg Ile Met Lys Ile Leu Asn His Pro Asn Ile Val Lys
65 70 75 80

Leu Phe Glu Val Ile Glu Thr Glu Lys Thr Leu Tyr Leu Val Met Glu
85 90 95

Tyr Ala Ser Gly Gly Glu Val Phe Asp Tyr Leu Val Ala His Gly Arg
100 105 110

Met Lys Glu Lys Glu Ala Arg Ala Lys Phe Arg Gln Ile Val Ser Ala
115 120 125

Val Gln Tyr Cys His Gln Lys Tyr Ile Val His Arg Asp Leu Lys Ala
130 135 140

Glu Asn Leu Leu Leu Asp Gly Asp Met Asn Ile Lys Ile Ala Asp Phe
145 150 155 160

Gly Phe Ser Asn Glu Phe Thr Val Gly Asn Lys Leu Asp Thr Phe Cys
165 170 175

Gly Ser Pro Pro Tyr Ala Ala Pro Glu Leu Phe Gln Gly Lys Lys Tyr
180 185 190

Asp Gly Pro Glu Val Asp Val Trp Ser Leu Gly Val Ile Leu Tyr Thr
195 200 205

Leu Val Ser Gly Ser Leu Pro Phe Asp Gly Gln Asn Leu Lys Glu Leu
210 215 220

Arg Glu Arg Val Leu Arg
225 230

<210> 12
<211> 230
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:GenBank G01025
kinase "homologue" domain

<400> 12
Ile Arg Gly Arg Asn Ser Ala Thr Ser Ala Asp Glu Gln Pro His Ile
1 5 10 15

Gly Asn Tyr Arg Leu Leu Lys Thr Ile Gly Lys Gly Asn Phe Ala Lys
20 25 30

Val Lys Leu Ala Arg His Ile Leu Thr Gly Lys Glu Val Ala Val Lys
35 40 45

Ile Ile Asp Lys Thr Gln Leu Asn Ser Ser Ser Leu Gln Lys Leu Phe
50 55 60

Arg Glu Val Arg Ile Met Lys Val Leu Asn His Pro Asn Ile Val Lys
65 70 75 80

Leu Phe Glu Val Ile Glu Thr Glu Lys Thr Leu Tyr Leu Val Met Glu
85 90 95

Tyr Ala Ser Gly Gly Glu Val Phe Asp Tyr Leu Val Ala His Gly Arg
100 105 110

Met Lys Glu Lys Glu Ala Arg Ala Lys Phe Arg Gln Ile Val Ser Ala
115 120 125

Val Gln Tyr Cys His Gln Lys Phe Ile Val His Arg Asp Leu Lys Ala
130 135 140

Glu Asn Leu Leu Leu Asp Ala Asp Met Asn Ile Lys Ile Ala Asp Phe
145 150 155 160

Gly Phe Ser Asn Glu Phe Thr Phe Gly Asn Lys Leu Asp Thr Phe Cys
165 170 175

Gly Ser Pro Pro Tyr Ala Ala Pro Glu Leu Phe Gln Gly Lys Lys Tyr
180 185 190

Asp Gly Pro Glu Val Asp Val Trp Ser Leu Gly Val Ile Leu Tyr Thr
195 200 205

Leu Val Ser Gly Ser Leu Pro Phe Asp Gly Gln Asn Leu Lys Glu Leu
210 215 220

Arg Glu Arg Val Leu Arg
225 230

<210> 13
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:GenBank P51954
kinase "homologue" domain

<400> 13
Met Glu Lys Tyr Val Arg Leu Gln Lys Ile Gly Glu Gly Ser Phe Gly
1 5 10 15

Lys Ala Val Leu Val Lys Ser Thr Glu Asp Gly Arg His Tyr Val Ile
 20 25 30

 Lys Glu Ile Asn Ile Ser Arg Met Ser Asp Lys Glu Arg Gln Glu Ser
 35 40 45

 Arg Arg Glu Val Ala Val Leu Ala Asn Met Lys His Pro Asn Ile Val
 50 55 60

 Gln Tyr Lys Glu Ser Phe Glu Glu Asn Gly Ser Leu Tyr Ile Val Met
 65 70 75 80

 Asp Tyr Cys Glu Gly Gly Asp Leu Phe Lys Arg Ile Asn Ala Gln Lys
 85 90 95

 Gly Ala Leu Phe Gln Glu Asp Gln Ile Leu Asp Trp Phe Val Gln Ile
 100 105 110

 Cys Leu Ala Leu Lys His Val His Asp Arg Lys Ile Leu His Arg Asp
 115 120 125

 Ile Lys Ser Gln Asn Ile Phe Leu Thr Lys Asp Gly Thr Val Gln Leu
 130 135 140

 Gly Asp Phe Gly Ile Ala Arg Val Leu Asn Ser Thr Val Glu Leu Ala
 145 150 160

 Arg Thr Cys Ile Gly Thr Pro Tyr Tyr Leu Ser Pro Glu Ile Cys Glu
 165 170 175

 Asn Lys Pro Tyr Asn Asn Lys Ser Asp Ile Trp Ala Leu Gly Cys Val
 180 185 190

 Leu Tyr Glu Leu Cys Thr Leu Lys His Ala Phe Glu Ala Gly Asn Met
 195 200 205

 Lys Asn Leu Val Leu Lys Ile Ile Ser
 210 215

 <210> 14
 <211> 233
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Mkinase kinase
 "homologue" domain

 <400> 14
 Met Trp Phe Phe Ala Arg Asp Pro Val Arg Asp Phe Pro Phe Glu Leu
 1 5 10 15

 Ile Pro Glu Pro Pro Glu Gly Gly Leu Pro Gly Pro Trp Ala Leu His
 20 25 30

 Arg Gly Arg Lys Lys Ala Thr Gly Ser Pro Val Ser Ile Phe Val Tyr
 35 40 45

 Asp Val Lys Pro Gly Ala Glu Glu Gln Thr Gln Val Ala Lys Ala Ala
 50 55 60

Phe Lys Arg Phe Lys Thr Leu Arg His Pro Asn Ile Leu Ala Tyr Ile
65 70 75 80

Asp Gly Leu Glu Thr Glu Lys Cys Leu His Val Val Thr Glu Ala Val
85 90 95

Thr Pro Leu Gly Ile Tyr Leu Lys Ala Arg Val Glu Ala Gly Gly Leu
100 105 110

Lys Glu Leu Glu Ile Ser Trp Gly Leu His Gln Ile Val Lys Ala Leu
115 120 125

Ser Phe Leu Val Asn Asp Cys Ser Leu Ile His Asn Asn Val Cys Met
130 135 140

Ala Ala Val Phe Val Asp Arg Ala Gly Glu Trp Lys Leu Gly Gly Leu
145 150 155 160

Asp Tyr Met Tyr Ser Ala Gln Gly Asn Gly Gly Pro Pro Arg Lys
165 170 175

Gly Ile Pro Glu Leu Glu Gln Tyr Asp Pro Pro Glu Leu Ala Asp Ser
180 185 190

Ser Gly Arg Val Val Arg Glu Lys Trp Ser Ala Asp Met Trp Arg Leu
195 200 205

Gly Cys Leu Ile Trp Glu Val Phe Asn Gly Pro Leu Pro Arg Ala Ala
210 215 220

Ala Leu Arg Asn Pro Gly Lys Ile Pro
225 230

<210> 15

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:kinase
"homologue" domain consensus peptide

<400> 15

Gly Ser Pro Val
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<210> 16

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:kinase
"homologue" domain consensus peptide

<400> 16

Asp Arg Ala Gly
1

<210> 17
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:kinase
"homologue" domain consensus peptide

<400> 17
Gly Cys Leu Ile
1

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